



SEQUENCE LISTING

RECEIVED

OCT 03 2002

TECH CENTER 1600/2900

<110> Michael E. Mendelsohn

<120> METHOD FOR ASSAYING COMPOUNDS AFFECTING
CELL DIVISION

<130> 00398/506001

<140> 09/352,570

<141> 1999-07-13

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (618)

C1

<400> 1

atg	gct	ctg	cag	ctc	tcc	cgg	gag	cag	gga	atc	acc	ctg	cgc	ggg	agc	48
Met	Ala	Leu	Gln	Leu	Ser	Arg	Glu	Gln	Gly	Ile	Thr	Leu	Arg	Gly	Ser	
1		5				10						15				

gcc	gaa	atc	gtg	gcc	gag	ttc	ttc	tca	ttc	ggc	atc	aac	agc	att	tta	96
Ala	Glu	Ile	Val	Ala	Glu	Phe	Phe	Ser	Phe	Gly	Ile	Asn	Ser	Ile	Leu	
20			25					30								

tat	cag	cgt	ggc	ata	tat	cca	tct	gaa	acc	ttt	act	cga	gtg	cag	aaa	144
Tyr	Gln	Arg	Gly	Ile	Tyr	Pro	Ser	Glu	Thr	Phe	Thr	Arg	Val	Gln	Lys	
35				40					45							

tac	gga	ctc	acc	ttg	ctt	gta	act	act	gat	ctt	gag	ctc	ata	aaa	tac	192
Tyr	Gly	Leu	Thr	Leu	Leu	Val	Thr	Thr	Asp	Leu	Glu	Leu	Ile	Lys	Tyr	
50				55					60							

cta	aat	aat	gtg	gtg	gaa	caa	ctg	aaa	gat	tgg	tta	tac	aag	tgt	tca	240
Leu	Asn	Asn	Val	Val	Glu	Gln	Leu	Lys	Asp	Trp	Leu	Tyr	Lys	Cys	Ser	
65			70				75					80				

gtt	cag	aaa	ctg	gtt	gta	gtt	atc	tca	aat	att	gaa	agt	ggg	gag	gtc	288
Val	Gln	Lys	Leu	Val	Val	Ile	Ser	Asn	Ile	Glu	Ser	Gly	Glu	Val		
85				90					95							

ctg	gaa	aga	tgg	cag	ttt	gat	att	gag	tgt	gac	aag	act	gca	aaa	gat	336
Leu	Glu	Arg	Trp	Gln	Phe	Asp	Ile	Glu	Cys	Asp	Lys	Thr	Ala	Lys	Asp	
100					105						110					

gac	agt	gca	ccc	aga	gaa	aag	tct	cag	aaa	gct	atc	cag	gat	gaa	atc	384
Asp	Ser	Ala	Pro	Arg	Glu	Lys	Ser	Gln	Lys	Ala	Ile	Gln	Asp	Glu	Ile	

115

120

125

cgt tca gtg atc aga cag atc aca gct acg gtg aca ttt ctg cca ctg 432
 Arg Ser Val Ile Arg Gln Ile Thr Ala Thr Val Thr Phe Leu Pro Leu
 130 135 140

ttg gaa gtt tct tgt tca ttt gat ctg ctg att tat aca gac aaa gat 480
 Leu Glu Val Ser Cys Ser Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp
 145 150 155 160

ttg gtt gta cct gaa aaa tgg gaa gag tcg gga cca cag ttt att acc 528
 Leu Val Val Pro Glu Lys Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr
 165 170 175

aat tct gag gaa gtg cgc ctt cgt tca ttt act act aca atc cac aaa 576
 Asn Ser Glu Glu Val Arg Leu Arg Ser Phe Thr Thr Ile His Lys
 180 185 190

gta aat agc atg gtg gcc tac aaa att cct gtc aat gac tga 618
 Val Asn Ser Met Val Ala Tyr Lys Ile Pro Val Asn Asp *
 195 200 205

C1
 <210> 2
 <211> 199
 <212> PRT
 <213> Homo sapiens

<400> 2
 Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu Ile Val Ala Glu
 1 5 10 15
 Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln Arg Gly Ile Tyr
 20 25 30
 Pro Ser Glu Thr Phe Thr Arg Val Gln Lys Tyr Gly Leu Thr Leu Leu
 35 40 45
 Val Thr Thr Asp Leu Glu Leu Ile Lys Tyr Leu Asn Asn Val Val Glu
 50 55 60
 Gln Leu Lys Asp Trp Leu Tyr Lys Cys Ser Val Gln Lys Leu Val Val
 65 70 75 80
 Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu Glu Arg Trp Gln Phe
 85 90 95
 Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser Ala Pro Arg Glu
 100 105 110
 Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser Val Ile Arg Gln
 115 120 125
 Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu Glu Val Ser Cys Ser
 130 135 140
 Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val Val Pro Glu Lys
 145 150 155 160
 Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser Glu Glu Val Arg
 165 170 175
 Leu Arg Ser Phe Thr Thr Ile His Lys Val Asn Ser Met Val Ala
 180 185 190
 Tyr Lys Ile Pro Val Asn Asp
 195

<210> 3
<211> 600
<212> DNA
<213> Ovis aries

<220>
<221> CDS
<222> (1)...(600)

<400> 3
cg₁ g₂ a₃ g₄ c₅ a₆ t₇ c₈ a₉ c₁₀ t₁₁ g₁₂ c₁₃ g₁₄ g₁₅ a₁₆ g₁₇ c₁₈ g₁₉ a₂₀ t₂₁ c₂₂ g₂₃ g₂₄ c₂₅ g₂₆ a₂₇ t₂₈ c₂₉ g₃₀ g₃₁ c₃₂ g₃₃ a₃₄ t₃₅ 48
Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu Ile Val Ala Glu
1 5 10 15
t₃₆ t₃₇ t₃₈ t₃₉ g₄₀ t₄₁ c₄₂ a₄₃ t₄₄ c₄₅ a₄₆ g₄₇ t₄₈ a₄₉ t₅₀ c₅₁ a₅₂ g₅₃ t₅₄ g₅₅ c₅₆ a₅₇ t₅₈ a₅₉ t₆₀ 96
Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln Arg Gly Ile Tyr
20 25 30
c₆₁ c₆₂ t₆₃ g₆₄ a₆₅ a₆₆ t₆₇ t₆₈ a₆₉ c₇₀ g₇₁ a₇₂ g₇₃ a₇₄ a₇₅ t₇₆ g₇₇ a₇₈ c₇₉ t₈₀ c₈₁ a₈₂ c₈₃ t₈₄ t₈₅ g₈₆ c₈₇ t₈₈ c₈₉ a₉₀ t₉₁ t₉₂ t₉₃ g₉₄ 144
Pro Ser Glu Thr Phe Thr Arg Val Gln Lys Tyr Gly Leu Thr Leu Leu
35 40 45
g₉₅ t₉₆ a₉₇ c₉₈ t₉₉ a₁₀₀ c₁₀₁ a₁₀₂ g₁₀₃ a₁₀₄ t₁₀₅ c₁₀₆ t₁₀₇ a₁₀₈ t₁₀₉ a₁₁₀ t₁₁₁ g₁₁₂ t₁₁₃ g₁₁₄ t₁₁₅ g₁₁₆ a₁₁₇ t₁₁₈ 192
Val Thr Thr Asp Pro Glu Leu Ile Lys Tyr Leu Asn Asn Val Val Asp
50 55 60
c₁₁₉ a₁₂₀ t₁₂₁ a₁₂₂ a₁₂₃ g₁₂₄ a₁₂₅ t₁₂₆ g₁₂₇ t₁₂₈ t₁₂₉ a₁₃₀ g₁₃₁ t₁₃₂ c₁₃₃ g₁₃₄ a₁₃₅ a₁₃₆ t₁₃₇ g₁₃₈ g₁₃₉ t₁₄₀ g₁₄₁ a₁₄₂ t₁₄₃ 240
Gln Leu Lys Glu Trp Leu Tyr Lys Cys Ser Val Gln Lys Leu Val Val
65 70 75 80
g₁₄₄ t₁₄₅ a₁₄₆ t₁₄₇ c₁₄₈ a₁₄₉ a₁₅₀ t₁₅₁ g₁₅₂ a₁₅₃ g₁₅₄ t₁₅₅ g₁₅₆ t₁₅₇ c₁₅₈ t₁₅₉ g₁₆₀ a₁₆₁ t₁₆₂ 288
Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu Glu Arg Trp Gln Phe
85 90 95
g₁₆₃ a₁₆₄ t₁₆₅ g₁₆₆ a₁₆₇ g₁₆₈ t₁₆₉ g₁₇₀ a₁₇₁ c₁₇₂ a₁₇₃ c₁₇₄ t₁₇₅ g₁₇₆ a₁₇₇ g₁₇₈ a₁₇₉ a₁₈₀ 336
Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser Ala Pro Arg Glu
100 105 110
a₁₈₁ a₁₈₂ g₁₈₃ t₁₈₄ c₁₈₅ a₁₈₆ g₁₈₇ a₁₈₈ t₁₈₉ c₁₉₀ c₁₉₁ g₁₉₂ t₁₉₃ a₁₉₄ t₁₉₅ a₁₉₆ g₁₉₇ a₁₉₈ c₁₉₉ g₂₀₀ 384
Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser Val Ile Arg Gln
115 120 125
a₂₀₁ t₂₀₂ c₂₀₃ a₂₀₄ c₂₀₅ a₂₀₆ t₂₀₇ t₂₀₈ c₂₀₉ c₂₁₀ t₂₁₁ g₂₁₂ t₂₁₃ g₂₁₄ a₂₁₅ g₂₁₆ t₂₁₇ t₂₁₈ t₂₁₉ t₂₂₀ c₂₂₁ a₂₂₂ 432
Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu Glu Val Ser Cys Ser
130 135 140
t₂₂₃ g₂₂₄ a₂₂₅ t₂₂₆ c₂₂₇ t₂₂₈ a₂₂₉ t₂₃₀ a₂₃₁ c₂₃₂ a₂₃₃ g₂₃₄ a₂₃₅ t₂₃₆ c₂₃₇ g₂₃₈ t₂₃₉ g₂₄₀ a₂₄₁ a₂₄₂ a₂₄₃ 480
Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val Val Pro Glu Lys
145 150 155 160
t₂₄₄ g₂₄₅ a₂₄₆ g₂₄₇ t₂₄₈ c₂₄₉ g₂₅₀ a₂₅₁ c₂₅₂ a₂₅₃ g₂₅₄ t₂₅₅ a₂₅₆ t₂₅₇ c₂₅₈ t₂₅₉ g₂₆₀ a₂₆₁ a₂₆₂ g₂₆₃ t₂₆₄ 528
Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser Glu Glu Val Arg
165 170 175
c₂₆₆ c₂₆₇ t₂₆₈ t₂₆₉ a₂₇₀ c₂₇₁ a₂₇₂ t₂₇₃ c₂₇₄ a₂₇₅ a₂₇₆ g₂₇₇ a₂₇₈ t₂₇₉ a₂₈₀ g₂₈₁ c₂₈₂ a₂₈₃ c₂₈₄ t₂₈₅ 576
Leu Arg Ser Phe Thr Thr Ile His Lys Val Asn Ser Met Val Ala
180 185 190

tac aaa att cct gtc cat gac tga 600
 Tyr Lys Ile Pro Val His Asp *
 195

<210> 4
<211> 199
<212> PRT
<213> Ovis aries

<400> 4
 Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu Ile Val Ala Glu
 1 5 10 15
 Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln Arg Gly Ile Tyr
 20 25 30
 Pro Ser Glu Thr Phe Thr Arg Val Gln Lys Tyr Gly Leu Thr Leu Leu
 35 40 45
 Val Thr Thr Asp Pro Glu Leu Ile Lys Tyr Leu Asn Asn Val Val Asp
 50 55 60
 Gln Leu Lys Glu Trp Leu Tyr Lys Cys Ser Val Gln Lys Leu Val Val
 65 70 75 80
 Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu Glu Arg Trp Gln Phe
 85 90 95
 Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser Ala Pro Arg Glu
 100 105 110
 Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser Val Ile Arg Gln
 115 120 125
 Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu Glu Val Ser Cys Ser
 130 135 140
 Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val Val Pro Glu Lys
 145 150 155 160
 Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser Glu Glu Val Arg
 165 170 175
 Leu Arg Ser Phe Thr Thr Ile His Lys Val Asn Ser Met Val Ala
 180 185 190
 Tyr Lys Ile Pro Val His Asp
 195

<210> 5
<211> 1458
<212> DNA
<213> Mus musculus

<400> 5
 atggcattct acagtctgc tggatgaaac tacagtgttc ccaggcgcac cggtaacctg 60
 gaagggtgggc ctgttcgcca gactgcaagc ccaaattgtgc tatggccaaac ttctggacac 120
 ctctctcctt tagccaccca ctgccaatca tcgcttctt atgcagaacc tcaaaagagt 180
 ccttggtgtg aagcaagatc actagaacac accttgccctg taaacagaga gaccctgaag 240
 aggaagcttgc gcgccggccgg ttgtgccagc cctgttacta gtccaaagc ac caagaggat 300
 gctcacttctt gtgccgtctg cagtgattat gcatctgggt atcattacgg tgtctggtcc 360
 tggatgaaatgtt gtaaggcatt tttaaaaga agcattcaag gacataatga ctatatctgt 420
 ccagccacga atcagtgtac gatagacaag aaccggcgta aaaactgcca ggcctgccc 480
 cttcgcaagt gttacgaaatgtt gggatggc aagtgtggat ccaggagaga aaggtgtggg 540
 taccgaatag tacgaagaca gagaagtgcg agcgagcagg tgcattgcctt gaacaaagcc 600
 aagagaacca gtgggcacac accccgggtt aaggagctac tgctgaactc tctgagtccc 660
 gagcagctgg tgctcaccct gctgaaatgtt gagccaccca atgtgcttagt gagtcgtccc 720
 agcatgcctt tcaccgaggc ctccatgtatg atgtccctta cgaagctggc tgacaaggaa 780

ctggtgacata tgattggctg ggccaagaaa atccctggct ttgtggagct cagcctgtt 840
 gaccaagtcc gcctcttgg aagctgctgg atggaggtgc tgatgggtgg gctgatgtgg 900
 cgctccatcg accaccccccgg caagctcatc tttgcctccag acctcggtct ggacaggat 960
 gaggggaagt gcgtggagg gattctggaa atcttgaca tgctcctggc gacgacggca 1020
 cggttccgtg agttaaaact gcagcacaaa gaatatctgt gtgtgaaggc catgattctc 1080
 ctcaactcca gtatgtacca ctggctacc gcaagccagg aagcagagag tagccggaa 1140
 ctgacacacc tattgaacgc agtgcacat gccctggct gggtgatttc gaagagtaga 1200
 atcttccc agcagcagtc agtccgtctg gccaacctcc tgatgcttct ttctcatgtc 1260
 aggacacatca gtaacaaggg catggAACat ctgctcagca tgaagtgcAA aaatgtggtc 1320
 ccggtgtacg acctgtgtct ggagatgctg aatgctcaca cgcttcgagg gtacaagtcc 1380
 tcaatctcggtt ggtctgggtt ctgctcagca gaggacagta agagcaaaga gggctccca 1440
 aacctccaggctcactgtca 1458

<210> 6
 <211> 485
 <212> PRT
 <213> Mus musculus

<400> 6
 Met Ala Phe Tyr Ser Pro Ala Val Met Asn Tyr Ser Val Pro Ser Ser
 1 5 10 15
 Thr Gly Asn Leu Glu Gly Gly Pro Val Arg Gln Thr Ala Ser Pro Asn
 20 25 30
 Val Leu Trp Pro Thr Ser Gly His Leu Ser Pro Leu Ala Thr His Cys
 35 40 45
 Gln Ser Ser Leu Leu Tyr Ala Glu Pro Gln Lys Ser Pro Trp Cys Glu
 50 55 60
 Ala Arg Ser Leu Glu His Thr Leu Pro Val Asn Arg Glu Thr Leu Lys
 65 70 75 80
 Arg Lys Leu Gly Gly Ser Gly Cys Ala Ser Pro Val Thr Ser Pro Ser
 85 90 95
 Thr Lys Arg Asp Ala His Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser
 100 105 110
 Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe
 115 120 125
 Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Ile Cys Pro Ala Thr Asn
 130 135 140
 Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Asn Cys Gln Ala Cys Arg
 145 150 155 160
 Leu Arg Lys Cys Tyr Glu Val Gly Met Val Lys Cys Gly Ser Arg Arg
 165 170 175
 Glu Arg Cys Gly Tyr Arg Ile Val Arg Arg Gln Arg Ser Ala Ser Glu
 180 185 190
 Gln Val His Cys Leu Asn Lys Ala Lys Arg Thr Ser Gly His Thr Pro
 195 200 205
 Arg Val Lys Glu Leu Leu Leu Asn Ser Leu Ser Pro Glu Gln Leu Val
 210 215 220
 Leu Thr Leu Leu Glu Ala Glu Pro Pro Asn Val Leu Val Ser Arg Pro
 225 230 235 240
 Ser Met Pro Phe Thr Glu Ala Ser Met Met Met Ser Leu Thr Lys Leu
 245 250 255
 Ala Asp Lys Glu Leu Val His Met Ile Gly Trp Ala Lys Lys Ile Pro
 260 265 270
 Gly Phe Val Glu Leu Ser Leu Leu Asp Gln Val Arg Leu Leu Glu Ser
 275 280 285
 Cys Trp Met Glu Val Leu Met Val Gly Leu Met Trp Arg Ser Ile Asp
 290 295 300
 His Pro Gly Lys Leu Ile Phe Ala Pro Asp Leu Val Leu Asp Arg Asp

305 310 315 320
Glu Gly Lys Cys Val Glu Gly Ile Leu Glu Ile Phe Asp Met Leu Leu
325 330 335
Ala Thr Thr Ala Arg Phe Arg Glu Leu Lys Leu Gln His Lys Glu Tyr
340 345 350
Leu Cys Val Lys Ala Met Ile Leu Leu Asn Ser Ser Met Tyr His Leu
355 360 365
Ala Thr Ala Ser Gln Glu Ala Glu Ser Ser Arg Lys Leu Thr His Leu
370 375 380
Leu Asn Ala Val Thr Asp Ala Leu Val Trp Val Ile Ser Lys Ser Arg
385 390 395 400
Ile Ser Ser Gln Gln Ser Val Arg Leu Ala Asn Leu Leu Met Leu
405 410 415
Leu Ser His Val Arg His Ile Ser Asn Lys Gly Met Glu His Leu Leu
420 425 430
Ser Met Lys Cys Lys Asn Val Val Pro Val Tyr Asp Leu Leu Leu Glu
435 440 445
Met Leu Asn Ala His Thr Leu Arg Gly Tyr Lys Ser Ser Ile Ser Gly
450 455 460
Ser Gly Cys Cys Ser Thr Glu Asp Ser Lys Ser Lys Glu Gly Ser Gln
465 470 475 480
Asn Leu Gln Ser Gln
485

C |
<210> 7
<211> 42
<212> PRT
<213> Mus musculus

<400> 7
Gly Ser Arg Arg Glu Arg Cys Gly Tyr Arg Ile Val Arg Arg Gln Arg
1 5 10 15
Ser Ala Ser Glu Gln Val His Cys Leu Asn Lys Ala Lys Arg Thr Ser
20 25 30
Gly His Thr Pro Arg Val Lys Glu Leu Leu
35 40
